

FIG. 1A

Input file ftmzb48h10; Output File ftmzb48h10.pat
Sequence length 3637

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GTGACCCACGGTCCGCACTCAACAATGCCTGCCCTCTCTGACTGCACCGTCCCGCCGCGCTGCCGCGCGCGCC 79
CAAGCCAAGTCGAGGGGGCGTTGCCACCGACGGCACAGCCCTTGGGCCCGCCCGGACACAGGAGGTGAGCCGCGCG 158
CGCACAGCTCCGTGCGCTCGCCCGTCTGAGCGCCCGCCAGGTGCCCCGACGCCCGCGCGCGAG ATG CAC AGC CCG 233
M H S P 4
P G L L A L W L C A V L C A S A R G G S 24
CCT GGG CTC CTG GCG CTG TGG CTT TGC GCT GTG CTG TGC GCA TCG GCG CGC GGC GGC AGC 293
D P Q P G P G R P A C P A P C H C Q E D 44
GAC CCC CAG CCT GGC CCG CCG GGT CCC GGT TGC CCG GCT CCC TGC CAC TGC CAG GAG GAC 353
G I M L S A D C S E L G L S V V P A D L 64
GGC ATC ATG CTG TCC GCT GAC TGC TCC GAG CTC GGG CTC TCA GTG GTG CCT GCG GAC CTG 413
D P L T A Y L D L S M N N L T E L Q P G 84
GAC CCC CTG ACG GCT TAC CTA GAC CTC AGT ATG AAC AAC CTC ACG GAG CTT CAG CCG GGT 473
L F H H L R F L E E L R L S G N H L S H 104
CTC TTC CAC CAC CTG CGC TTC CTG GAG GAG CTG CGG CTC TCA GGC AAC CAC CTC TCA CAC 533
I P G Q A F S G L H S L K I L M L Q S N 124
ATC CCG GGA CAG GCA TTC TCC GGC CTC CAC AGC CTC AAA ATT CTA ATG CTG CAG AGC AAC 593

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FIG.1B

Q	L	R	G	I	P	A	E	A	L	W	E	L	P	S	L	Q	S	L	R	144
CAG	CTC	CGT	GGG	ATC	CCA	GCA	GAG	GCA	CTA	TGG	GAG	CTG	CCC	AGC	CTG	CAG	TCG	CTG	CGC	653
L	D	A	N	L	I	S	L	V	P	E	R	S	F	E	G	L	S	S	L	164
CTA	GAT	GCT	AAT	CTC	ATC	TCC	CTG	GTC	CCT	GAG	AGA	AGC	TTT	GAG	GGG	CTC	TCC	TCC	CTC	713
R	H	L	W	L	D	D	N	A	L	T	E	I	P	V	R	A	L	N	N	184
CGC	CAC	CTC	TGG	CTG	GAT	GAC	AAT	GCA	CTC	ACT	GAG	ATC	CCC	GTC	AGA	GCT	CTC	AAC	AAC	773
L	P	A	L	Q	A	M	T	L	A	L	N	H	I	R	H	I	P	D	Y	204
CTT	CCT	GCC	CTA	CAG	GCC	ATG	ACC	TTG	GCT	CTC	AAC	CAT	ATC	CGC	CAC	ATC	CCT	GAC	TAT	833
A	F	Q	N	L	T	S	L	V	V	L	H	L	H	N	N	R	I	Q	H	224
GCC	TTC	CAG	AAC	CTC	ACC	AGT	CTT	GTG	GTG	CTG	CAT	CTA	CAT	AAC	AAC	CGC	ATC	CAG	CAT	893
V	G	T	H	S	F	E	G	L	H	N	L	E	T	L	D	L	N	Y	N	244
GTG	GGG	ACC	CAC	AGC	TTC	GAG	GGG	CTG	CAC	AAT	CTG	GAG	ACA	CTA	GAC	CTG	AAC	TAT	AAT	953
E	L	Q	E	F	P	L	A	I	R	T	L	G	R	L	Q	E	L	G	F	264
GAG	CTG	CAG	GAG	TTC	CCC	TTG	GCT	ATC	CGG	ACC	CTG	GGC	AGG	CTG	CAG	GAA	TTG	GGT	TTC	1013
H	N	N	N	I	K	A	I	P	E	K	A	F	M	G	N	P	L	L	Q	284
CAT	AAC	AAC	AAC	ATC	AAG	GCT	ATC	CCA	GAG	AAA	GCC	TTC	ATG	GGC	AAC	CCT	CTC	CTG	CAG	1073
T	I	H	F	Y	D	N	P	I	Q	F	V	G	R	S	A	F	Q	Y	L	304
ACA	ATA	CAT	TTT	TAT	GAC	AAC	CCA	ATC	CAG	TTT	GTG	GGA	AGG	TCA	GCA	TTC	CAG	TAC	CTG	1133

FIG. 1C

S	K	L	H	T	L	S	L	N	G	A	T	D	I	Q	E	F	P	D	L	324
TCT	AAA	CTG	CAT	ACG	CTA	TCT	TTG	AAT	GGT	GCC	ACT	GAT	ATC	CAA	GAG	TTC	CCA	GAC	CTC	1193
K	G	T	T	S	L	E	I	L	T	L	T	R	A	G	I	R	L	L	P	344
AAA	GGC	ACC	ACT	AGC	CTG	GAG	ATC	CTG	ACC	CTG	ACC	CGT	GGC	GGC	ATC	AGA	CTG	CTC	CCA	1253
P	G	V	C	Q	Q	L	P	R	L	R	I	L	E	L	S	H	N	Q	I	364
CCG	GGA	GTG	TGC	CAA	CAG	CTG	CCT	AGG	CTC	CGA	ATC	CTG	GAG	CTG	TCT	CAT	AAT	CAG	ATC	1313
E	E	L	P	S	L	H	R	C	Q	K	L	E	E	I	G	L	R	H	N	384
GAG	GAG	TTA	CCC	AGC	CTG	CAC	AGA	TGT	CAG	AAG	CTG	GAG	GAA	ATT	GGC	CTC	CGA	CAT	AAC	1373
R	I	K	E	I	G	A	D	T	F	S	Q	L	G	S	L	Q	A	L	D	404
AGG	ATC	AAG	GAA	ATT	GGT	GCA	GAT	ACC	TTT	AGC	CAG	CTG	GGC	TCC	TTG	CAA	GCT	TTA	GAC	1433
L	S	W	N	A	I	R	A	I	H	P	E	A	F	S	T	L	R	S	L	424
CTG	AGT	TGG	AAT	GCC	ATC	CGT	GCC	ATC	CAC	CCT	GAG	GCT	TTC	TCA	ACC	CTT	CGA	TCC	TTG	1493
V	K	L	D	L	T	D	N	Q	L	T	T	L	P	L	A	G	L	G	G	444
GTT	AAG	CTG	GAC	CTG	ACT	GAC	AAC	CAG	CTG	ACC	ACA	CTG	CCC	CTG	GCT	GGG	CTG	GGA	GGC	1553
L	M	H	L	K	L	K	G	N	L	A	L	S	Q	A	F	S	K	D	S	464
CTG	ATG	CAC	CTG	AAG	CTC	AAA	GGG	AAC	TTG	GCC	CTG	TCT	CAG	GCC	TTC	TCC	AAG	GAC	AGT	1613
F	P	K	L	R	I	L	E	V	P	Y	A	Y	Q	C	C	A	Y	G	I	484
TTC	CCA	AAA	CTG	AGG	ATC	CTG	GAG	GTG	CCC	TAC	GCC	TAC	CAG	TGC	TGT	GCC	TAC	GGC	ATC	1673

FIG.1D

C	A	S	F	F	K	T	S	G	Q	W	Q	A	E	D	F	H	P	E	E	504
TGT	GCC	AGC	TTC	TTC	AAG	ACC	TCT	GGG	CAG	TGG	CAG	GCC	GAG	GAC	TTT	CAT	CCA	GAA	GAA	1733
E	E	A	P	K	R	P	L	G	L	L	A	G	Q	A	E	N	H	Y	D	524
GAG	GAG	GCA	CCA	AAG	AGG	CCC	CTG	GGT	CTC	CTT	GCT	GGA	CAA	GCT	GAG	AAC	CAC	TAT	GAC	1793
L	D	L	D	E	L	Q	M	G	T	E	D	S	K	P	N	P	S	V	Q	544
CTA	GAC	CTG	GAT	GAG	CTC	CAG	ATG	GGG	ACA	GAG	GAC	TCA	AAG	CCA	AAC	CCC	AGT	GTC	CAG	1853
C	S	P	V	P	G	P	F	K	P	C	E	H	L	F	E	S	W	G	I	564
TGC	AGC	CCT	GTT	CCA	GGC	CCC	TTC	AAG	CCC	TGC	GAG	CAC	CTC	TTT	GAG	AGC	TGG	GGC	ATC	1913
R	L	A	V	W	A	I	V	L	L	S	V	L	C	N	G	L	V	L	L	584
CGC	CTT	GCT	GTG	TGG	GCC	ATC	GTG	CTG	CTC	TCC	GTA	CTC	TGT	AAC	GGG	CTG	GTG	CTG	CTG	1973
T	V	F	A	S	G	P	S	P	L	S	P	V	K	L	V	V	G	A	M	604
ACA	GTC	TTT	GCC	AGC	GGA	CCC	AGC	CCG	CTG	TCC	CCC	GTC	AAG	CTT	GTG	GTG	GGT	GCG	ATG	2033
A	G	A	N	A	L	T	G	I	S	C	G	L	L	A	S	V	D	A	L	624
GCA	GGC	GCC	AAC	GCC	CTG	ACG	GGC	ATT	TCC	TGT	GGT	CTC	CTG	GCC	TCT	GTG	GAC	GCC	TTG	2093
T	Y	G	Q	F	A	E	Y	G	A	R	W	E	S	G	L	G	C	Q	A	644
ACC	TAT	GGT	CAG	TTC	GCT	GAG	TAT	GGA	GCC	CGC	TGG	GAG	AGC	GGT	CTG	GGC	TGC	CAG	GCT	2153
T	G	F	L	A	V	L	G	S	E	A	S	V	L	L	L	T	L	A	A	664
ACG	GGC	TTC	CTG	GCT	GTC	CTG	GGT	TCA	GAG	GCG	TGG	GTG	CTG	CTG	CTC	ACA	CTG	GCG	GCC	2213

FIG. 1E

V	Q	C	S	I	S	V	T	C	V	R	A	Y	G	K	A	P	S	P	G	684
GTG	CAG	TGC	AGC	ATC	TCT	GTG	ACC	TGC	GTC	CGA	GCC	TAC	GGG	AAG	GCG	CCG	TCG	CCT	GGC	2273
S	V	R	A	G	A	L	G	C	L	A	L	A	G	L	A	A	A	L	P	704
AGC	GTC	CGC	GCA	GGC	GCA	CTG	GGA	TGC	CTG	GCG	CTG	GCC	GGG	CTG	GCC	GCA	GCA	CTG	CCG	2333
L	A	S	V	G	E	Y	G	A	S	P	L	C	L	P	Y	A	P	P	E	724
CTG	GCC	TCG	GTG	GGA	GAG	TAT	GGC	GCC	TCC	CCA	CTC	TGC	CTG	CCC	TAC	GCC	CCA	CCC	GAG	2393
G	R	P	A	A	L	G	F	A	V	A	L	V	M	M	N	S	L	C	F	744
GGC	CGG	CCG	GCC	GCC	CTG	GGC	TTC	GCT	GTA	GCC	CTG	GTG	ATG	ATG	AAC	TCG	CTC	TGC	TTC	2453
L	V	V	A	G	A	Y	I	K	L	Y	C	D	L	P	R	G	D	F	E	764
CTG	GTG	GTG	GCC	GCC	TAC	TAC	ATC	AAG	CTC	TAC	TGT	GAC	CTG	CCA	CGG	GGT	GAC	TTT	GAG	2513
A	V	W	D	C	A	M	V	R	H	V	A	W	L	I	F	A	D	G	L	784
GCC	GTG	TGG	GAC	TGC	GCC	ATG	GTG	CGC	CAC	GTG	GCC	TGG	CTC	ATC	TTT	GCA	GAT	GGC	CTC	2573
L	Y	C	P	V	A	F	L	S	F	A	S	M	L	G	L	F	P	V	T	804
CTC	TAC	TGC	CCC	GTG	GCC	TTC	CTC	AGC	TTT	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACC	2633
P	E	A	V	K	S	V	L	L	V	V	L	P	L	P	A	C	L	N	P	824
CCC	GAG	GCT	GTC	AAG	TCA	GTC	CTT	CTG	GTG	GTG	CTG	CCT	CTG	CCT	GCC	TGC	CTC	AAC	CCA	2693
L	L	Y	L	L	F	N	P	H	F	R	D	D	L	R	R	L	W	P	S	844
CTG	CTC	TAC	CTG	CTC	TTC	AAC	CCT	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CTC	TGG	CCA	AGC		2753

FIG. 1F

P R S P G P L A Y A A A G E L E K S S C 864
CCT CGG TCC CCA GGG CCC CTA GCC TAC GCT GCT GCA GCC GGT GAG CTG GAG AAG AGC TCC TGC 2813

D S T Q A L V A F S D V D L I L E A S E 884
GAC TCC ACC CAA GCG CTG GTG GCT TTC TCA GAT GTG GAT CTT ATT CTG GAA GCT TCT GAG 2873

A G Q P P G L E T Y G F P S V T L I S R 904
GCT GGG CAG CCT CCT GGG CTA GAG ACC TAT GGC TTC CCT TCA GTG ACC CTC ATC TCC CGA 2933

H Q P G A T R L E G N H F I E S D G T K 924
CAT CAG CCG GGG GCC ACC AGG CTG GAG GGA AAC CAT TTT ATA GAG TCT GAT GGA ACC AAG 2993

F G N P P Q P P M K G E L L K A E G A T 944
TTT GGG AAC CCA CAA CCT CCC ATG AAG GGA GAA CTG CTG CTG AAG GCA GAG GGA GCC ACT 3053

L A G C G S S V G G A L W P S G S L F A 964
TTG GCA GGC TGT GGC TCT TCC GTG GGT GGA GCC CTC TGG CCC TCT GGC TCT CTC TTT GCC 3113

S H L * 968
TCT CAC TTG TAA 3125

ATATCCCTCTCTGTTGTCTCTCTCCCATCCAAATGATGGCTGCTTATAAAGAAAGACAACCTCCAACCTCAGCAAGA 3204

TGGCCAAACACCTCTGACTCCATTGTTCTCTCTCCACGACCCCTAACCAATGAGTGCTTCCAAGTCTTGCTTTGTCTTGG 3283

CCTTCAGCTTCACTTTCACCCCTGGCCCTTCTCTGTCTCAATCCAAATACCTTCTGACAGAGGCCCTGGGAAATTTGCATAGGA 3362

FIG.1G

GAAAGGAGAAAAGCAAAGACAGTGAAGGTTATTGGGCCCTGACAGAGCCATGATCAGTAAGTGCAGAGTGATGGGAG 3441

GTCTCACAGAGCATGACACTGGAAGACAACCTACCAAAGACATTGGAGAGTCTCCCCCTGTGACATATAGAATATAAAATG 3520

TGTTCTGCCGTTCCATTAAATCTTGACCTATGCTGNGGCCAAAGTGCTTCCTGTAAATAACACTTTGGAAGACATTGAAAA 3599

AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3637

??

FIG. 2A

LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnLk<-
 +LdLs N+Lt+l pg++++L+ Leel Ls+N+L+++p ++f++L+
 ftmzb048h1
 67 LTAYLDLSMNNLTQLPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH 114

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnLk<-
 +L+ L L+ N+L+++p++a|+ Lp+L++L L+ N ++ +p++++f++L+
 ftmzb048h1
 115 SLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSEGLS 162

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnLk<-
 +L++L+L++N Lt++p al+nLp L+ L N+++++p++++fqnL+
 ftmzb048h1
 163 SLRHLWDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLT 210

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnL k<-
 +L +L+L nN+++++ ++++++L+nLe+LdL++N+L+++p ++L+
 ftmzb048h1
 211 SLVVLHLHNNRIQHVGTSHSFEGLNLETLDLNYNELQEFPL-AIRTLG 257

FIG.2B

LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+eL + nN+++ +p+ a+ + p L+++++ +N ++ + ++fq L+
ftmzb048h1
258 RLQELGFHNNNIKAIPKAFMGNPLLQTIHFYDNPIQFVGRSAFYLS 305

LRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L++L+L++ ++++++p+ |++ ++Le L L + ++ lppg++q L+
ftmzb048h1
306 KLHTLSLNGATdIQEFPD--LKGTTSLEILTLTRAGIRLLPPGVCCQLP 352

LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+ L+Ls+N++++lp+ |+ +++Lee+ L +N+++++ ++f+ L+
ftmzb048h1
353 RLRILELSHNQIEELPS--LHRCQKLEELGRHNRIKEIGADTFSQLG 398

LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+lp + +L
ftmzb048h1
399 SLQALDLSWNAIRAIHPEAFSTLRSVLKDLTDNQLTTLPLAGLGGLM 446

FIG. 3A-1

Protein (species)*	Function-ligand	Location
RNase inhibitor (porcine)	RNase inhibitor-RNase	Cytoplasm
Leucine-rich $\alpha 2$ -GP (human)	?-?	Serum
RNA1 (Saccharomyces cerevisiae)	RNA processing-?	Cytoplasm
U2 snRNP A' (human)	Splicing-U2 snRNP	Nucleus
Biglycan (human)	ECM binding-laminin, fibronectin, TGF- β	ECM
Decorin (human)	ECM binding-collagen, fibronectin, thrombospondin, TGF- β	ECM
Fibromodulin (bovine)	ECM binding-collagen, fibronectin	ECM
Lumican (chicken)	Corneal transparency-?	ECM
Proteoglycan-Lb (chicken)	?-?	ECM
Osteoinductive factor (bovine)	Bone morphogenesis-BMP	ECM
Platelet GP ba (human)	Cell adhesion-WF, thrombin	PM (EC)
Platelet GP V (human)	Cell adhesion-GP IX, GP Ib	PM (EC)
YopM (Yersinia pestis)	Virulence factor-thrombin	IC + EC
IpaH7.8 (Shigella flexnen)	?-?	?
IpaH4.5 (Shigella flexnen)	?-?	?
Toll (Drosophilla)	Embryo development-?	PM (EC)
Silt (Drosophilla)	Axon development-?	EC
Connectin (Drosophilla)	Synapse development-?	PM (EC)
Chaoptin (Drosophilla)	Photoreceptor-cell development-?	PM (EC)
Flightless-1 (Drosophilla)	Embryo development-?	PM (EC)
Oligodendrocyte myelin GP (human)	Myelination-?	PM (EC)

FIG. 3A-2

Repeats	Length	Consensus sequence	PIR entry
15	28 (A)	.LE.L.L..C-.LT...C..L..aL....	A31857
	29 (B)	.L.EL.L..N-.LGD.Ga..L..L..P..	
8	24	.L..L.L..N-.L..-L...LL....--	NBHUA2
8	29	.L..L.L..N-.a.....a.....	BVBYN1
4	24	.L..L.a..N-.a.....L--	S03616
8	24	.L..L.L..N-.I..-a.....a....--	A40757
10	24	.L..L.L..N-.I..-V.....a....--	NBHUC8
11	24	.L..L.L..N-.a..-a.....a....--	S05390
12	24	.L..L.L..N-.L..-.....a....--	A41748
6	24	.L..a.L..N-.I..-.....a....--	A41781
6	24	.L..a.L..N-.a..-.....F....--	A35272
7	24	.L..L.L..N-.L..-LP.GL...L--	NBHUIA
14	24	.L..L.L..N-.L..-LP..LF..L--	-
12	20	.L..L.a..N-.L..-LP-....L--PP	A33950
6	20	.L..L.V..N-.L..-LP-....L--P.	A35149
8	20	.L..L.a..N-.L..-LP-....L--P.	S18248
19	24	.L..L.L..N-.L..-.....F....--	A29943
19	24	.L..L.L..N-.I..-.....F..L--	A36665
7	24	.L..LNL..N-.I..-a....aF..L--	S28464
30	24	.L..L.L..N-.a..-a.....F..a--	A29944
16	23	.L..L.LS.N-.L..-aP..a..-L--	-
8	24	.L..L.LSNN-.a..-a.....L--	A34210

FIG. 3B-1

Protein (species)*	Function-ligand	Location
CD14 (human)	Cell-surface receptor-LPS-LPB	PM (EC)
Trk (human)	Receptor protein kinase-NGF	PM (EC)
TrkB (mouse)	Receptor protein kinase-BDNF,	PM (EC)
TrkC (porcine)	Receptor protein kinase-NT-3	PM (EC)
TMK1 (Arabidopsis thaliana)	Receptor protein kinase-?	PM (EC)
LH-CG receptor (rat)	Signal transduction-LH, CG	PM (EC)
PSH receptor (rat)	Signal transduction-PSH	PM (EC)
TSH receptor (dog)	Signal transduction-TSH	PM (EC)
Adenylate cyclase (Saccharomyces Cerevisiae)	Signal transduction-RAS	PM (cytoplasm)
T-LR (Tyrpanosoma brucei)	?-?	?
RAD1 (Saccharomyces cerevisiae)	DNA repair-RAD10	Nucleus
RAD7 (Saccharomyces cerevisiae)	DNA repair-?	?
DRT100 (Arabidopsis thaliana)	Recombination-?	Chloroplast
GRR1 (Saccharomyces cerevisiae)	Signal transduction-?	Cytoplasm
CCR4 (Saccharomyces cerevisiae)	Transcription-?	?
sds22 (Schizosaccharomyces pombe)	Mitosis-dis2, sds21	Nucleus
p34 ribosome-binding protein (rat)	RM membranes-ribosome	RM membrane (cytoplasm)
Carboxypeptidase N (human)	Stabilization-catalytic subunit	Plasma
Intermalin (Listeria monocytogenes)	Invasion-?	Cell wall
InIB (Listeria monocytogenes)	?-?	?
LRR superfamily		

FIG. 3B-2

Repeats	Length	Consensus sequence	PIR entry
8	27	.a..L.L..N-.....	TDHUM4
2	23	.L..L.IS.N-.L.....	TVHUTT
3	23	.L..L.aT.N-.LTS.....	S06943
3	23	.LR.aNLSQN-.L...S-.....	A40026
11	23	.L..a.L..N-...G.aP-..a.SL--.	JQ1674
5	25	.L..L.a..T-.a.....F.....	A41343
7	25	.L..L.aS.T-....LP...a..a--.	A34548
6	25	.a..L.a.NN..a.S-a.....a....	A40077
20	23	.L..L.L..N-.a..-a....-a..L--.	OYBY
18	23	.L..L.LSGC..a..-a..-a..L--.	A36359
3	23	.a.LaDI..N--LP..a.....N----	DDBYD1
5	26	.L..L.a..C..a.....a....-P	A25226
5	24	.L..LNL..N-.L.G.IP.S-a.S.--.	A46260
9	26	.L..a.L..C.NaTD..a..-L..L.-.	A41529
4	23	.L..L.a..N-.LT.-LP.E-a.....	S31286
11	22	.L..L.a..N-.I..-a--ENa..L--.	A38439
4	24	.L..LDL..N-.L..-LP....F..L--.	-
12	24	.L..L.L..N-.L..-LP...aF..L--.	A34901
13	22	NL..L.L..n-QISDI.P---L..L--T	A39930
6	22	.L..L.L..N-.L.DI...-L..L--.	C39930
	5 10 15 20 25	.L..L.L..N*.a..*a****a**a**.	

FIG. 4

>human DNA seq.

TAATACGACTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAA
TTCCCGGGTTCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCC
GGCTCATCCAGCCTCTCTTGCTGCCCTAGCGGCCTCCAACACAACCGCATCTG
GGAAATTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATC
TTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCAC
TCCCTGGTCAAGCTGGACCTGACAGACAACCAGCTGACCACACTGCCCCTGGC
TGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCC
AGGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATG
CCTACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG
CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCC
CCTGGGCCTCCTTGCCAGACAAGCAGAGAACCCTATGACCAGGACCTGGATG
AGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAGC
CCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTGAAAGCTGGGGCAT
CCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGG
TGCTGCTGACCGTGTTTCGCTGGCGGGCCTGCCCCCCTGCCCCCGGTCAAGTTT
GTGGTAGGTGCGATTGCAGGCGCCAACACCTTGACTGGCATTTCCTGTGGCCT
TCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCC
GCTGGGAGACGGGGCTAGGCTGCCGGGGCCACTGGCTTCCTGGCAGTACTTGG
GTCGGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCAGTGCAGTGCAGCGTC
TCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCC
AGCAGGGGTCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCAGTCCCC
CTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGC
CACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAT
GAACTCCTTCTGTTTCCTGGTTCGTGGCCGGTGCCTACATCAAAGTGTACTGTGA
CCTGCCCGGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC
GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCT
CAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCCGAGGCCGTCAAGT
CTGTCTGCTGGTGGTGTGCTGCCCCCTGCCTGCCTGCCTCAACCCACTGCTGTAC
CTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCGCGC
AGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGC
TCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTG
GAAGCTTCTGAAGCTGGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC
AGTGACCCTCATCTCCTGTGAGCAGCCAGGGGGCCCCCAGGCTGGAGGGCAGC
CATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCTCCATGGA
TGGAGAAGTGTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTG
TCAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTGTA
AATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCTCTCCCCCTCG
GTGAATGATGGCTGCTTCTAAAACAAATACAACCAAACTCAGCAGTGTGATCT
ATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCAT
CACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCT
TGATACTGGGCCTCTTCCCTTGTGATGTCTGAAGCTGTGGACCAGAGACCTGGAC
TTTTGTCTGCTTAAGGGAAATGAGGGAAAGTAAAGACAGTGAAGGGGTGGAGGG
TTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGT
GATTTCCCGTGTGACTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAT
CTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATT
AAAAAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGATCCAAGCTTACGTACGCGT
GCATGCGACGTCATAGCTCTTCTATAGTGTACCTAAATTCAATT

FIG. 5

>fahr human

NTTHYRESWYACRYRGIPGSTHASVERSQGLSLPAHPASLAALAASNTTASGKLE
DTFSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHL
KLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDLHLD
DEESSKRPLGLLARQAEENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPC EYL
FESWGIRLAWAIVLLSVLCNGLVLLTVFAGGPAPLPVKFVVGAIAGANTLTGISCG
LLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSEASVLLLTAAVQC SVSVS
CVRAYGKSPSLGSRAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQP
AALGFTVALVMMNSFCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAVLIFAD
GLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVPLPACLNPLL YLLFNPHFRDDL R
RLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRP PGLETYG
FPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELL LRAEGSTPAGGGL
SGGGGFQPSGLAFASHV

FIG. 6

LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11

*->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnL
+L+ LdLs N ++s++p+a+s+L++L +LdL +N+Lt+lp + +L

fahr 64 SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTNDNQLTTLPLAGLGGL 110

k<*

fahr 111 M 111

FIG. 7A

ftmzb048h10	1	MHSPGGLALWLCASARGSDPQPGGRPACAPCHQEDGIMLSADCSELGLSVVPADLDPLTAYLDLSMNLTE	80
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	
ftmzb048h10	81	LQGLFHHRLFEELRLSGNHLSHIPGQAFSGLSKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPSRFEG	160
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	
ftmzb048h10	161	LSSLRHLWDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLTSLVVLHLNNRIQHVGTHSFEGHLNLETLD	240
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	
ftmzb048h10	241	LNYNELQEFFLAIRTLGRLQELGFHNNNIKAPEKAFMGNPLLOTIHFYDNPIQFVGRSAFQYLSKLHTLSLNGATDIOE	320
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	
ftmzb048h10	321	FPDLKGTTSLEILTLAGIRLLPPGVCQQLPRLRILELSHNQIEELPSLHRCQKLEELGLRHNRIKEIGADTFSQLGSL	400
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	
ftmzb048h10	401	QALDLSWNAIRAIHPEAFSTLRSVLKDLTDNQLTTPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC	480
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	
ftmzb048h10	481	AYGICASFCKTSGQWQAEDEHPEEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPGPFKPCHEHLFE	560
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	

FIG. 7B

561	ftmzb048h10	561	640	640
Aa_of_aambb001d112	SWGIRLAVWAIVLLSVLCNGLVLLTVFASGSPSPSPVKLVVGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGL			
fahr_human	SWGIRLAVWAIVLLSVLCNGLVLLTVFASGSPSPSPVKLVVGAMAGANALSGISCGLLASVDALTYGQFAEYGARWESGL			
	SWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPVPKFWVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGL			
		I	TM II	
		641	720	720
ftmzb048h10	GCQATGFLAVLGSEASVLLLTAAVQCSISVTCVRAVGKAPSPGSGVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY			
Aa_of_aambb001d112	GCQATGFLAVLGSEASVLLLTAAVQCSISVTCVRAVGKAPSPGSGVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY			
fahr_human	GCQATGFLAVLGSEASVLLLTAAVQCSISVTCVRAVGKAPSPGSGVRAGVLCALAGLAAALPLASVGEYGASPLCLPY			
		TM III	TM IV	
		721	800	800
ftmzb048h10	APPEGRPAALGFAVALVMNNSLCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAVWLIFADGLLYCPVAFLSFASMLGL			
Aa_of_aambb001d112	APPEGRPAALGFAVALVMNNSLCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAVWLIFADGLLYCPVAFLSFASMLGL			
fahr_human	APPEGRPAALGFTVALVMNNSFCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAVWLIFADGLLYCPVAFLSFASMLGL			
		TM V	TM VI	
		801	880	880
ftmzb048h10	FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRLWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL			
Aa_of_aambb001d112	FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRLWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL			
fahr_human	FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRLWPSPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL			
		TM VII		
		881	960	960
ftmzb048h10	EASEAGQPPGLETYGFPSVTILSRHQPGATRLIEGNHFIESDGTKFGNPQPPMKGELLKKAEGATLAGCGSSVGGALWPSG			
Aa_of_aambb001d112	EASEAGQPPGLETYGFPSVTILSRHQPGATRLIEGNHFIESDGTKFGNPQPPMKGELLKKAEGATLAGCGSSVGGALWPSG			
fahr_human	EASEAGRPPGLETYGFPSVTILSCQPGAPRLIEGSHCHVEPEGNHFGNPQPSMDGELLILRAEGSTPAGGCLSGGGGFQPSG			
		961	968	968
ftmzb048h10	SLFASHLN			
Aa_of_aambb001d112	SLFASHLN			
fahr_human	LAFASHVN			

FIG.8A

G	L	H	N	L	E	T	L	D	L	N	Y	N	K	L	Q	E	F	P	V	20
GGG	CTG	CAC	AAT	CTG	GAG	ACA	CTA	GAC	CTG	AAT	TAT	AAC	AAG	CTG	CAG	GAG	TTC	CCT	GTG	60
A	I	R	T	L	G	R	L	Q	E	L	G	F	H	N	N	N	I	K	A	40
GCC	ATC	CGG	ACC	CTG	GGC	AGA	CTG	CAG	GAA	CTG	GGG	TTC	CAT	AAC	AAC	AAC	ATC	AAG	GCC	120
I	P	E	K	A	F	M	G	N	P	L	L	Q	T	I	H	F	Y	D	N	60
ATC	CCA	GAA	AAG	GCC	TTC	ATG	GGG	AAC	CCT	CTG	CTA	CAG	ACG	ATA	CAC	TTT	TAT	GAT	AAC	180
P	I	Q	F	V	G	R	S	A	F	Q	Y	L	P	K	L	H	T	L	S	80
CCA	ATC	CAG	TTT	GTG	GGA	AGA	TCG	GCA	TTC	CAG	TAC	CTG	CCT	AAA	CTC	CAC	ACA	CTA	TCT	240
L	N	G	A	M	D	I	Q	E	F	P	D	L	K	G	T	T	S	L	E	100
CTG	AAT	GGT	GCG	ATG	GAC	ATC	CAG	GAG	TTT	CCA	GAT	CTC	AAA	GGC	ACC	ACC	AGC	CTG	GAG	300
I	L	T	L	T	R	A	G	I	R	L	L	P	S	G	M	C	Q	Q	L	120
ATC	CTG	ACC	CTG	ACC	CGC	GCA	GGC	ATC	CGG	CTG	CTC	CCA	TCG	GGG	ATG	TGC	CAA	CAG	CTG	360
P	R	L	R	V	L	E	L	S	H	N	Q	I	E	E	L	P	S	L	H	140
CCC	AGG	CTC	CGA	GTC	CTG	GAA	CTG	TCT	CAC	AAT	CAA	ATT	GAG	GAG	CTG	CCC	AGC	CTG	CAC	420
R	C	Q	K	L	E	E	I	G	L	Q	H	N	R	I	W	E	I	G	A	160
AGG	TGT	CAG	AAA	TTG	GAG	GAA	ATC	GGC	CTC	CAA	CAC	AAC	CGC	ATC	TGG	GAA	ATT	GGA	GCT	480
D	T	F	S	Q	L	S	S	L	Q	A	L	D	L	S	W	N	A	I	R	180
GAC	ACC	TTC	AGC	CAG	CTG	AGC	TCC	CTG	CAA	GCC	CTG	GAT	CTT	AGC	TGG	AAC	GCC	ATC	CGG	540

FIG.8B

S I H P E A F S T L H S L V K L D L T D 200
TCC ATC CAC CCT GAG GCC TTC TCC ACC CTG CAC TCC CTG GTC AAG CTG GAC CTG ACA GAC 600

N Q L T T L P L A G L G G L M H L K L K 220
AAC CAG CTG ACC ACA CTG CCC CTG GCT GGA CTT GGG GGC TTG ATG CAT CTG AAG CTC AAA 660

G N L A L S Q A F S K D S F P K L R I L 240
GGG AAC CTT GCT CTC TCC CAG GCC TTC TCC AAG GAC AGT TTC CCA AAA CTG AGG ATC CTG 720

E V P Y A Y Q C C P Y G M C A S F F K A 260
GAG GTG CCT TAT GCC TAC CAG TGC TGT CCC TAT GGG ATG TGT GCC AGC TTC TTC AAG GCC 780

S G Q W E A E D L H L D D E E S S K R P 280
TCT GGG CAG TGG GAG GCT GAA GAC CTT CAC CTT GAT GAT GAG GAG TCT TCA AAA AGG CCC 840

L G L L A R Q A E N H Y D Q D L D E L Q 300
CTG GGC CTC CTT GCC AGA CAA GCA GAG AAC CAC TAT GAC CAG GAC CTG GAT GAG CTC CAG 900

L E M E D S K P H P S V Q C S P T P G P 320
CTG GAG ATG GAG GAC TCA AAG CCA CAC CCC AGT GTC CAG TGT AGC CCT ACT CCA GGC CCC 960

F K P C E Y L F E S W G I R L A V W A I 340
TTC AAG CCC TGT GAG TAC CTC TTT GAA AGC TGG GGC ATC CGC CTG GGC GTG TGG GCC ATC 1020

V L L S V L C N G L V L L L T V F A G G P 360
GTG TTG CTC TCC GTG CTC TGC AAT GGA CTG GTG CTG CTG ACC GTG TTC GCT GGC GGC CCT 1080

FIG. 8C

```
A P L P P V K F V V G A I A G A N T L T 380
GCC CCC CTG CCC CCG GTC AAG TTT GTG GTA GGT GCG ATT GCA GGC AAC ACC TTG ACT 1140

G I S C G L L A S V D A L T F G Q F S E 400
GGC ATT TCC TGT GGC CTT CTA GCC TCA GTC GAT GCC CTG ACC TTT GGT CAG TTC TCT GAG 1200

Y G A R W E T G L G C R A T G F L A V L 420
TAC GGA GCC CGC TGG GAG ACG GGG CTA GGC TGC CGG GCC ACT GGC TTC CTG GCA GTA CTT 1260

G S E A S V L L L L T L A A V Q C S V S V 440
GGG TCG GAG GCA TCG GTG CTG CTG CTC ACT CTG GCC GCA GTG CAG TGC AGC GTC TCC GTC 1320

S C V R A Y G K S P S L G S V R A G V L 460
TCC TGT GTC CGG GCC TAT GGG AAG TCC CCC TCC CTG GGC AGC GTT CGA GCA GGC GTC CTA 1380

G C L A L A G L A A A L P L A S V G E Y 480
GGC TGC CTG GCA CTG GCA GGC CTG GCC GCA CTG CCC CTG GCC TCA GTG GGA GAA TAC 1440

G A S P L C L P Y A P P P E G Q P A A L G 500
GGG GCC TCC CCA CTC TGC TGC CCC TAC GCG CCA CCT GAG GGT CAG CCA GCA GCC CTG GGC 1500

F T V A L V M N S F C F L V V A G A Y 520
TTC ACC GTG GCC CTG GTG ATG ATG AAC TCC TTC TGT TTT CTG GTC GTG GCC GGT GCC TAC 1560

I K L Y C D L P R G D F E A V W D C A M 540
ATC AAA CTG TAC TGT GAC CTG CCG CGG GGC GAC TTT GAG GCC GTG TGG GAC TGC GCC ATG 1620
```

FIG. 8D

V	R	H	V	A	W	L	I	F	A	D	G	L	L	Y	C	P	V	A	F	560
GTG	AGG	CAC	GTG	GCC	TGG	CTC	ATC	TTC	GCA	GAC	GGG	CTC	CTC	TAC	TGT	CCC	GTG	GCC	TTC	1680
L	S	F	A	S	M	L	G	L	F	P	V	T	P	E	A	V	K	S	V	580
CTC	AGC	TTC	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACG	CCC	GAG	GCC	GTC	AAG	TCT	GTC	1740
L	L	V	V	L	P	L	P	A	C	L	N	P	L	L	Y	L	L	F	N	600
CTG	CTG	GTG	GTG	CTG	CCC	CTG	CCT	GCC	TGC	CTC	AAC	CCA	CTG	CTG	TAC	CTG	CTC	TTC	AAC	1800
P	H	F	R	D	D	L	R	R	L	R	P	R	A	G	D	S	G	P	L	620
CCC	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CGG	CTT	CGG	CCC	CGC	GCA	GGG	GAC	TCA	GGG	CCC	CTA	1860
A	Y	A	A	A	G	E	L	E	K	S	S	C	D	S	T	Q	A	L	V	640
GCC	TAT	GCT	GCG	GCC	GGG	GAG	CTG	GAG	AAG	AGC	TCC	TGT	GAT	TCT	ACC	CAG	GCC	CTG	GTA	1920
A	F	S	D	V	D	L	I	L	E	A	S	E	A	G	R	P	P	G	L	660
GCC	TTC	TCT	GAT	GTG	GAT	CTC	ATT	CTG	GAA	GCT	TCT	GAA	GCT	GGG	CGG	CCC	CCT	GGG	CTG	1980
E	T	Y	G	F	P	S	V	T	L	I	S	C	Q	Q	P	G	A	P	R	680
GAG	ACC	TAT	GGC	TTC	CCC	TCA	GTG	ACC	CTC	ATC	TCC	TGT	CAG	CAG	CCA	GGG	GCC	CCC	AGG	2040
L	E	G	S	H	C	V	E	P	E	G	N	H	F	G	N	P	Q	P	S	700
CTG	GAG	GGC	AGC	CAT	TGT	GTA	GAG	CCA	GAG	GGG	AAC	CAC	TTT	GGG	AAC	CCC	CAA	CCC	TCC	2100
M	D	G	E	L	L	L	R	A	E	G	S	T	P	A	G	G	G	L	S	720
ATG	GAT	GGA	GAA	CTG	CTG	CTG	AGG	GCA	GAG	GGA	TCT	ACG	CCA	GCA	GGT	GGA	GGC	TTG	TCA	2160

G	G	G	G	F	Q	P	S	G	L	A	F	A	S	H	V	*
GGG	GGT	GGC	GGC	TTT	CAG	CCC	TCT	GGC	TTG	GCC	TTT	GCT	TCA	CAC	GTG	TAA
ATATCCCTCCCCATTCTTCTCTTCCCTCTCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTTAAAACA	2290															
AAATAACAACCAAACCTAGCAGTGATCTATAGCAGGATGCCCAGTACCCTGGCTCCACTGATCACCTCTCTCCTGTGA	2369															
CCATCACCAACGGGTGCCTCTTGGCCTTCCCTTGGCCTTCCCTCAGCTTCACCTTGATACTGGGCCCTCTTCCCTTG	2448															
TCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTTGTCTGTCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGG	2527															
TGGAGGGTTGATCAGGCCACAGTGGACAGGGAGACCCTCACAGAGAAGGCCCTGGAAGGTGATTTCCCGTGTGACTCATG	2606															
GATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATATGCATAAAGACTTCCTATTAAAAATAAGCTT	2685															
TGGAAGAGATTAAAAAATAAAAAAAAAA	2711															

FIG. 9

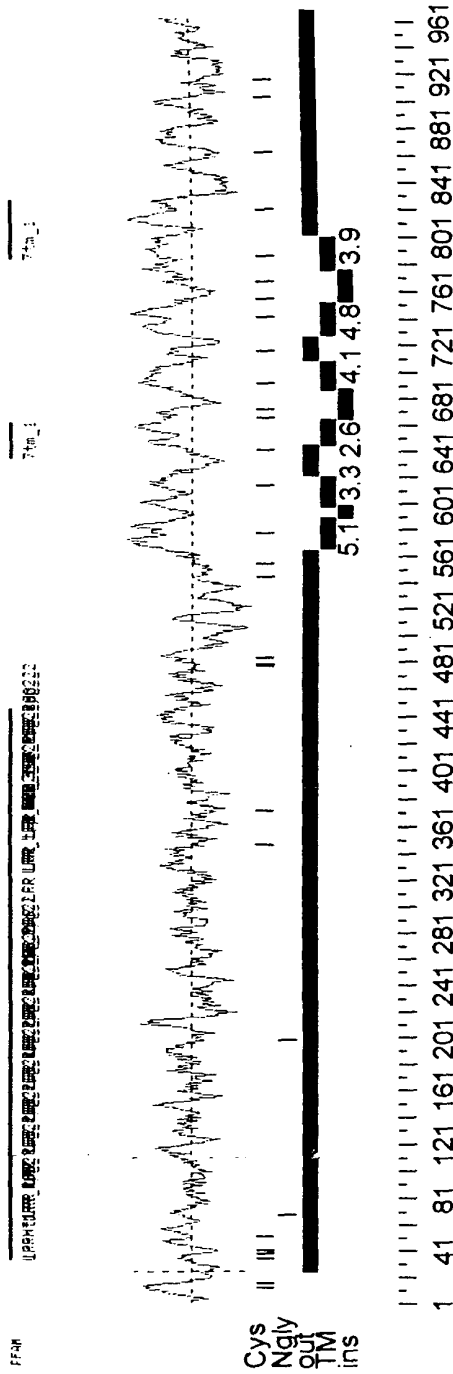


FIG. 10A

Searching for complete domains in PFAM

hmmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMM file: /prod/ddm/seqanal/PFAM/pfam6.2/Pfam

Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
<u>LRR</u>	Leucine Rich Repeat	241.4	1.3e-68	16
<u>LRRNT</u>	Leucine rich repeat N-terminal domain	27.2	0.00038	1
<u>7tm_1</u>	7 transmembrane receptor (rhodopsin family)	7.2	0.14	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
-------	--------	-------	-------	-------	-------	-------	---------

LRRNT	1/1	34	65 ..	1	31 []	27.2	0.00038
LRR	1/16	67	90 ..	1	23 []	12.4	11
LRR	2/16	91	114 ..	1	23 []	24.2	0.0031
LRR	3/16	115	138 ..	1	23 []	19.9	0.062
LRR	4/16	139	162 ..	1	23 []	16.4	0.7
LRR	5/16	163	186 ..	1	23 []	27.5	0.00031
LRR	6/16	187	210 ..	1	23 []	12.1	13
LRR	7/16	211	234 ..	1	23 []	21.6	0.019
LRR	8/16	235	257 ..	1	23 []	18.2	0.2
LRR	9/16	258	281 ..	1	23 []	19.0	0.11
LRR	10/16	282	305 ..	1	23 []	10.2	32
LRR	11/16	306	328 ..	1	23 []	5.6	1.5e+02
LRR	12/16	329	352 ..	1	23 []	8.8	52
LRR	13/16	353	374 ..	1	23 []	19.2	0.097
LRR	14/16	375	398 ..	1	23 []	16.9	0.49
LRR	15/16	399	422 ..	1	23 []	23.7	0.0042
LRR	16/16	423	446 ..	1	23 []	16.4	0.66
7tm_1	1/2	635	662 ..	51	79 ..	3.4	2.2
7tm_1	2/2	784	827 ..	207	259 .]	1.1	11

FIG. 10B

Alignments of top-scoring domains:

LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038

->aCpreCtCsp..fglvVdCsgrgLtleVPrdlP<-

aCp++C+C +++ l+ dCs++gL +vP dl

15088 34 ACPAPCHCQEdgIMLSADCSELGLS-AVPGDLD 65

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11

->nLeeLdLsnN.LtslppglfsnLp<-

+LdLs N+Lt+l pglf++L+

15088 67 LTAYLDLSMNnLTELPGLFHHLR 90

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031

->nLeeLdLsnN.LtslppglfsnLp<-

LeeL+Ls+N+L+++p +fs+L

15088 91 FLEELRLSGNnLSHIPGQAFSGLY 114

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062

->nLeeLdLsnN.LtslppglfsnLp<-

+L+ L L+nN+L ++p +++ Lp

15088 115 SLKILMLQNNqLGGIPAEALWELP 138

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L+L+ N ++ +p+ +f++L+

15088 139 SLQSLRLDANIISLVPERSFEGLS 162

LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L+L++N Lt++p +++nLp

15088 163 SLRHLWLDDNaLTEIPVRALNNLP 186

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13

->nLeeLdLsnN.LtslppglfsnLp<-

L+ L N+++++p+ +f+nL+

15088 187 ALQAMTLALNriSHIPDYAFQNL 210

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019

->nLeeLdLsnN.LtslppglfsnLp<-

+L +L+L+nN++++l ++f++L

15088 211 SLVVLHLHNNriQHLGTHSFEGH 234

FIG. 10C

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2

->nLeeLdLsnN.LtslppglfsnLp<-

nLe+LdL++N+L+++p +++ L

15088 235 NLETLDLNYNkLQEFV-AIRTLG 257

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11

->nLeeLdLsnN.LtslppglfsnLp<-

+L+eL ++nN+++ +p+++f+ p

15088 258 RLQELGFHNNnIKAIPEKAFMGNP 281

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32

->nLeeLdLsnN.LtslppglfsnLp<-

L+-----+N+++ + ++f+ Lp

15088 282 LLQTIHFYDNpIQFVGRSAFQYLP 305

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L+L++ +++++p+ +++ +

15088 306 KLHTLSLNGAmdIQEFPD--LKGTT 328

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52

->nLeeLdLsnN.LtslppglfsnLp<-

+Le L L + +++ lp+g +++Lp

15088 329 SLEILTLTRAgIRLLPSGMCQQLP 352

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L Ls+N++++lp+ ++ ++

15088 353 RLRVLELSHNqIEELPS--LHRCQ 374

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49

->nLeeLdLsnN.LtslppglfsnLp<-

+Lee+ L++N++ ++ ++fs+L+

15088 375 KLEEIGLQHNrIWEIGADTFSQLS 398

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042

->nLeeLdLsnN.LtslppglfsnLp<-

+L+ LdLs N ++s++p++fs L

15088 399 SLQALDLSWNaIRSIHPEAFSTLH 422

FIG. 10D

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66

->nLeeLdLsnN.LtslppglfsnLp<-

+L +LdL +N+Lt+lp ++L

15088 423 SLVKLDLTDNqLTTLPLAGLGGLM 446

7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2

->dWpfGsalCklvtaldvvnmyaSillLta<-

+W G ++C+ +++l v+ + aS+llLt+

15088 635 RWETG-LGCRATGFLAVLGSEASVLLLTL 662

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11

*->ICWiPyfivllldtlc.lsiimsstCelervlptallvtlwLayvNs

l+ P +++ +l ++ +++++++v l++ ++

15088 784 LLYCPVAFLSFASMLGIFPV-----

TPEAVKSVLLVVLPLPA 820

cINPiIY<-*

cINP++Y

15088 821 CLNPLLY 827

FIG. 11A

//

Searching for complete domains in SMART
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)
 Copyright (C) 1992-1998 Washington University School of Medicine
 HMMER is freely distributed under the GNU General Public License (GPL).
 HMM file: /ddm/robison/smart/smart.all.hmms
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR_typ_2		247.2	2.3e-70	14
LRR_PS_2		78.1	1.8e-19	13
LRR_sd22_2		33.5	4.9e-06	5
lrrnt1		25.7	0.0011	1
LRR_bac_2		11.8	3	7
LRR_RI_2		5.4	7.7	4

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
lrrnt1	1/1	34	70	1	38	25.7	0.0011
LRR_PS_2	1/13	64	87	1	24	1.9	1.2e+02
LRR_typ_2	1/14	64	88	1	24	12.6	2.1

FIG. 11B

LRR_bac_2	1/7	89	108	..	1	20	[]	0.9	80
LRR_PS_2	2/13	89	111	..	1	24	[]	17.2	0.4
LRR_typ_2	2/14	89	112	..	1	24	[]	32.1	1.3e-05
LRR_RI_2	1/4	89	115	..	1	28	[]	3.6	14
LRR_bac_2	2/7	113	132	..	1	20	[]	1.6	66
LRR_PS_2	3/13	113	136	..	1	24	[]	1.1	1.5e+02
LRR_typ_2	3/14	113	136	..	1	24	[]	19.2	0.1
LRR_bac_2	3/7	137	156	..	1	20	[]	0.1	1e+02
LRR_PS_2	4/13	137	159	..	1	24	[]	7.1	24
LRR_typ_2	4/14	137	160	..	1	24	[]	25.9	0.00095
LRR_PS_2	5/13	161	183	..	1	24	[]	11.4	6.6
LRR_typ_2	5/14	161	184	..	1	24	[]	27.5	0.00031
LRR_sd22_2	1/5	161	187	..	1	22	[]	5.3	31
LRR_RI_2	2/4	161	190	..	1	28	[]	5.3	8
LRR_PS_2	6/13	185	207	..	1	24	[]	7.0	25
LRR_typ_2	6/14	185	208	..	1	24	[]	23.2	0.0062
LRR_PS_2	7/13	209	232	..	1	24	[]	3.1	79
LRR_typ_2	7/14	209	232	..	1	24	[]	28.1	0.0002
LRR_RI_2	3/4	209	235	..	1	28	[]	1.2	31
LRR_sd22_2	2/5	209	235	..	1	22	[]	13.5	3
LRR_bac_2	4/7	233	252	..	1	20	[]	10.7	4.1
LRR_typ_2	8/14	233	255	..	1	24	[]	16.1	0.76
LRR_PS_2	8/13	233	255	..	1	24	[]	17.1	0.43
LRR_bac_2	5/7	256	275	..	1	20	[]	10.2	1e+02
LRR_PS_2	9/13	256	278	..	1	24	[]	2.9	85
LRR_typ_2	9/14	256	279	..	1	24	[]	24.4	0.0026

FIG. 11C

LRR_typ_2	10/14	327	350 ..	1	24 []	3.1	29
LRR_bac_2	6/7	351	370 ..	1	20 []	14.6	1.3
LRR_PS_2	10/13	351	372 ..	1	24 []	10.8	8
LRR_sd22_2	3/5	351	372 ..	1	22 []	7.6	16
LRR_typ_2	11/14	351	373 ..	1	24 []	18.8	0.13
LRR_RI_2	4/4	351	378 ..	1	28 []	2.6	19
LRR_PS_2	11/13	373	396 ..	1	24 []	2.3	1e+02
LRR_typ_2	12/14	374	396 ..	1	24 []	6.8	10
LRR_sd22_2	4/5	397	418 ..	1	22 []	7.0	19
LRR_PS_2	12/13	397	419 ..	1	24 []	13.6	3.4
LRR_typ_2	13/14	397	420 ..	1	24 []	30.4	4.3e-05
LRR_bac_2	7/7	421	440 ..	1	20 []	5.8	18
LRR_sd22_2	5/5	421	441 ..	1	22 []	3.7	49
LRR_PS_2	13/13	421	442 ..	1	24 []	5.5	39
LRR_typ_2	14/14	421	444 ..	1	24 []	21.6	0.018

Alignments of top-scoring domains:

lrrntl1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011

->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<-
+CPapC+C ++ ++ dCs++gL +vP dl + t +
15088 34 ACPAPCHCQEdGIMLSADCSELGLS--AVPGDLPLTAY 70

LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02

->LtsL.qvLdLsnNnLsGeIPsslgn<-
L L+ +LdLs NnL+ e+ + l+
15088 64 LDPLtAYLDLSMNNLT-ELQPGLFH 87

FIG. 11D

LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
 ->LpnL.reLdLsnNqLtsLPpgaFqg<-

L L+ LdLs N+Lt+L pg+F++
 15088 64 LDPLtAYLDLSMNNLTQLPGLFHH 88

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80

->PpsLkeLnvsnNrLteLPeL<-

+L+eL+ s+N+L+ P
 15088 89 LRFLEELRLSGNHLSHIPGQ 108

LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4

->LtsLqvLdLsnNnLsGeIPsslgn<-

L+ L++L+Ls+N+Ls +IP + ++
 15088 89 LRFLEELRLSGNHLs-HIPGQAFS 111

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05

->LpnLreLdLsnNqLtsLPpgaFqg<-

L+ L+eL+Ls+N+L+++P +aF+g
 15088 89 LRFLEELRLSGNHLSHIPGQAFSG 112

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14

->npsLreLdLsnNkl.gdeGaralaealks<-

++ L+eL+Ls+N+L+++ G + ++L s
 15088 89 LRFLEELRLSGNHLsHIPG--QAFSGLYS 115

FIG. 11E

LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
->PpsLkeLnvsnNrLteLPeL<-
 sLk+L +nN+L P+
15088 113 LYSLKILMLQNNQLGGIPAE 132

LRR_ps_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
->LtsLqvLdLsnNnLsGeIPsslgn<-
 L sL++L L+nN+L G +l+
15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
->LpnLreLdLsnNqLtsLPpgaFqg<-
 L +L+ L L+nNqL +P++a++
15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
->PpsLkeLnvsnNrLteLPeL<-
 psL++L+ +N ++ Pe
15088 137 LPSLQSLRLDANLISLVPER 156

LRR_ps_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sLq+L+L N +s +P+ +
15088 137 LPSLQSLRLDANLIS-LVPERSE 159

FIG. 11F

LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
 ->LpnLreLdsnNqLtsLppgaFqg<-
 Lp+L++L+L+ N ++ +P++ F+g
 15088 137 LPSLQSLRLDANLISLVPERSFEG 160

LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
 ->LtsLqvLdsnNnLsGeIPsslgn<-
 L+sL++L L +N L+ eIP n
 15088 161 LSSLRHLWLDNALT-EIPVRALN 183

LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031
 ->LpnLreLdsnNqLtsLppgaFqg<-
 L++Lr+L L++N+Lt++P +a+++
 15088 161 LSSLRHLWLDNALT-EIPVRALNN 184

LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
 ->LtnLeeLdlsqNkI.....kkIENLde<-
 L+ L++L+L +N +++ + + + NL
 15088 161 LSSLRHLWLDNALT-EIPVRALNNLPA 187

LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
 ->npsLreLdsnNklgdeGaraL..aeaLks<-
 ++sLr L+L +N l++ +raL++ aL++
 15088 161 LSSLRHLWLDNALT-EIPVRALnnLPALQA 190

FIG. 11G

LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+ Lq L+ N++s +IP+ ++
 15088 185 LPALQAMTLALNRIS-HIPDYAFQ 207

LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 Lp+L+ L N++++P+ aFq+
 15088 185 LPALQAMTLALNRISHIPDYAFQN 208

LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 LtsL+vL+L+nN++ s+
 15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232

LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L++L +L+L+nN++++L F+g
 15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232

LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31
 ->npsLreLdLsnNkligdeGaraLaealks<-
 ++sL +L+L nN + G + e+L+
 15088 209 LTSLVVLHLHNNRIQHLGTHSF-EGLHN 235

FIG. 11H

LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
 ->LtnLeeIdLsqNkI.....kKiENLde<-
 Lt L++L L +N+I++ +++++E+L++
 15088 209 LTSLVVLHLHNNRIqhlgtHSFEGLHN 235

LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
 ->PpsLkeLnvsNnRlLteLPeL<-
 ++L++L+ ++N+L e+P
 15088 233 LHNLETLDLNYNKLQEFPPVA 252

LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1, E = 0.76
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L+nL++LdL++N+L++ P + +
 15088 233 LHNLETLDLNYNKLQEFPPVAI-RT 255

LRR_ps_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L++L++LdL++N+L e+P +
 15088 233 LHNLETLDLNYNKLQ-EFPVAIRT 255

LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
 ->PpsLkeLnvsNnRlLteLPeL<-
 +L+eL+ nN+++ Pe
 15088 256 LGRLQELGFHNNNIKAIPeK 275

FIG. 11I

LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85
->LtsLqvLdLsnNnLsGeIPsslgn<-
L +Lq+L ++nNn+ IP+ +
15088 256 LGRLELGFHNNNIK-AIPEKAFM 278

LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026
->LpnLreLdLsnNqLtsLPpgaFqg<-
L+ L+eL +nN++++P+ aF g
15088 256 LGRLELGFHNNNIKAIPEKAFMG 279

LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29
->LpnLreLdLsnNqLtsLPpgaFqg<-
++L+ L L + ++ LP+g++q
15088 327 TTSLEILTLTRAGIRLLPSGMCQQ 350

LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3
->PpsLkeLnvsnNrLtelPeL<-
p+L+ L s+N+++eLP L
15088 351 LPRLRVLELSHNQIEELPSL 370

LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8
->LtsLqvLdLsnNnLsGeIPsslgn<-
L++L+vL+Ls+N++ e+Ps l +
15088 351 LPRLRVLELSHNQIE-ELPS-LHR 372

FIG. 11J

LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
 ->LtnLeeIdLsqNkIkIENLde<-
 L +L++L+Ls+N+I+ + L+
 15088 351 LPRLRVLELSHNQIEELPSLHR 372

LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
 ->LpnLreIdLsnNqLtsLPpgaFgg<-
 Lp Lr+L Ls+Nq++LP + ++
 15088 351 LPRLRVLELSHNQIEELP-SLHRC 373

LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
 ->npsLreIdLsnNkIgdGaraLaaLks<-
 +p+Lr+L Ls+N + + + ++ L++
 15088 351 LPRLRVLELSHNQIEELPSLHRCQKLEE 378

LRR_PS_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
 ->LtsLqvIdLsnNnLsGeIPsslgn<-
 +++L+++ L++N++ +++++
 15088 373 CQKLEEIGLQHNRIWEIGADTFSQ 396

LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
 ->LpnLreIdLsnNqLtsLPpgaFgg<-
 +L+e L++N++ ++ +++F+
 15088 374 -QKLEEIGLQHNRIWEIGADTFSQ 396

FIG. 11K

LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19
 -->LtnLeeLdLsqNkIkkiENLde<-
 L+ L+ LdLs+N I++i
 15088 397 LSSLQALDLSWNAIRSIHPEAF 418

LRR_PS_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4
 -->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sLq LdLs+N + +I ++ ++
 15088 397 LSSLQALDLSWNAIR-SIHPEAFS 419

LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05
 -->lpnlrelLdLsnNqLtsLPpgaFqg<-
 L++L+ LdLs+N+++s++p+aF+
 15088 397 LSSLQALDLSWNAIRSIHPEAFST 420

LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18
 -->PpsLkelnvsnNrLtelPeL<-
 +sL +L+ +N+Lt+LP
 15088 421 LHSLVKLDLTDNQLTTLPLA 440

LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49
 -->LtnLeeLdLsqNkIkkiENLde<-
 L+ L+ LdL +N+++ + L +
 15088 421 LHSLVKLDLTDNQLTTL-PLAG 441

FIG. 11L

LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sL+ LdL +N+L+ ++P g
 15088 421 LHSLVKLDLTDNQLT-TLPL-AGL 442

LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018
 ->LpnLrelDlsnNqLtsLPpgaFgg<-
 L++L +LdL +NqLt+LP ++g
 15088 421 LHSLVKLDLTDNQLTTLPLAGLGG 444

//

FIG.12A

GAP of: FrGcgManager_101_HTAUB3ha_ check: 2817 from: 1 to: 3637

mLGR6 - 1 (analysis only) - Import - complete

to: FrGcgManager_101_ITA0fLsO_ check: 3059 from: 1 to: 2711

corrected human LGR6 (analysis o - Import - complete

Symbol comparison table:

/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp

CompCheck: 8760

Gap Weight:	12	Average Match:	10.000
Length Weight:	4	Average Mismatch:	0.000

Quality:	21826	Length:	3688
Ratio:	8.051	Gaps:	20
Percent Similarity:	84.248	Percent Identity:	84.211

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	5
.	=	1

FIG. 12B

FrGcgManager_101_HTAUB3ha_ x FrGcgManager_101_ITA0fLsO_

```
901 CCCACAGCTTCGAGGGGCTGCACAAATCTGGAGACACTAGACCTGAACCTAT 950
    |||||
1  ..... GGGCTGCACAAATCTGGAGACACTAGACCTGAATTAT 36

951 AATGAGCTGCAGGAGTTCCTCCCTTGGCTATCCGGACCTGGGCAGACTGCA 1000
    || |||||
37 AACAAAGCTGCAGGAGTTCCTCTGTGGCCATCCGGACCTGGGCAGACTGCA 86

1001 AGAATTGGGTTTCCATAACAACAACATCAAGGCTATCCCAGAGAAAGCCT 1050
    ||| |||||
87 GGAAGTGGGGTTCCATAACAACAACATCAAGGCCATCCCAGAAAAGGCCT 136

1051 TCATGGGCAACCCCTCTCCTGCAGACAATACATTTTATGACAAACCCAATC 1100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
137 TCATGGGAAACCCCTCTGTCTACAGACGATACACTTTTATGATAACCCAATC 186

1101 CAGTTTGTGGGAAGGTCAGCATTCAGTACCTGTCTAAACTGCATACGCT 1150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
187 CAGTTTGTGGGAAGATCGGCATTCAGTACCTGCCTAAACTCCACACACT 236
```

11151 ATCTTTGAATGGTGCCACTGATATATCAAGAGTTCCAGACCTCAAAGGCA 1200
 237 ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGGCA 286
 11201 CCACCTAGCCTGGAGATCCTGACCCCTGACCCGTCGGGCATCAGACTGCTC 1250
 287 CCACCAAGCCTGGAGATCCTGACCCCTGACCCGCGCAGGCATCCGGCTGCTC 336
 11251 CCACCCGGGAGTGTGCCAACAGCTGCCCTAGGCTCCGAATCCTGGAGCTGTC 1300
 337 CCATCGGGGATGTGCCAACAGCTGCCCCAGGCTCCGAGTCTCGAACTGTC 386
 11301 TCATAATCAGATCGAGGAGTTACCCAGCCTGCACAGATGTCAGAAGCTGG 1350
 387 TCACAAATCAAAATTGAGGAGCTGCCCAGCCTGCACAGGTGTCAGAAATTGG 436
 11351 AGGAAATTGGCCTCCGACATAACAGGATCAAGGAAATTGGTGCAGATACC 1400
 437 AGGAAATCGGCCTCCAACACACACCCGCATCTGGGAAATTGGAGCTGACACC 486
 11401 TTCAGCCAGCTGGGCTCCTTGCAAGCTTTAGACCTGAGTTGGAATGCCAT 1450
 487 TTCAGCCAGCTGAGCTCCCTGTCAAGCCCTGGATCTTAGCTGGAACGCCAT 536
 11451 CCGTGCCATCCACCCTGAGGCTTTCTCAACCCCTTCGATCCTTGGTTAAGC 1500
 537 CCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACCTCCCTGGTCAAGC 586

FIG. 12D

1501 TGGACCTGACTGACAACCAGCTGACCACACTGCCCTGGCTGGCTGGGA 1550
|||||
587 TGGACCTGACAGACAACCAGCTGACCACACTGCCCTGGCTGGACTTGGG 636
1551 GGCCCTGATGCACCTGAAGCTCAAAGGGAACCTTGGCCCTGTCTCAGGCCCTT 1600
|||
637 GGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCCTT 686
1601 CTCCAAGGACAGTTTCCCAAACCTGAGGATCCTGGAGGTGCCCTACGCCT 1650
|||||
687 CTCCAAGGACAGTTTCCCAAACCTGAGGATCCTGGAGGTGCCCTTATGCCT 736
1651 ACCAGTGCTGTGCCCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCTGGG 1700
|||||
737 ACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGG 786
1701 CAGTGGCAGGCCGAGGACTTTCATCCAGAAGAAGAGGAGGCACCAAAGAG 1750
|||||
787 CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAG 836
1751 GCCCCCTGGGTCTCCTTGCTGGACAAGCTGAGAACCACTATGACCTAGACC 1800
|||||
837 GCCCCCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACC 886
1801 TGGATGAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCAGTGTC 1850
|||||
887 TGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACACCCAGTGTC 936

FIG. 12F

```
2201 CACACTGGCGCGCGTGCAGTGCAGCATCTCTGTGACCTGCGTCCGAGCCT 2250
    ||| |||| | | ||||| |||| | | |||| | |||| | ||||
1287 CACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTCTGTGTCGGGCCT 1336

2251 ACGGGAAGCGCGCGTCCCTGGCAGCGTCCGCGCAGGCGCACTGGGATGC 2300
    | |||| | | | | ||||| || ||||| | | || | ||
1337 ATGGGAAGTCCCCCTCCCTGGGCGAGCGTTCCGAGCAGGGGTCTTAGGCTGC 1386

2301 CTGGCGCTGGCGCGGCTGGCCGCGCAGCACTGCCGCTGGCCTCGGTGGGAGA 2350
    |||| | |||| | ||||| || ||||| || ||||| || ||||| ||
1387 CTGGCACTGGCAGGGCTGGCCGCGCGCACTGCCCTGGCCTCAGTGGGAGA 1436

2351 GTATGGCGCCTCCCCACTCTGCCTGCCCTACGCCCCACCCGAGGGCCGGC 2400
    || | | ||||| ||||| ||||| ||||| ||||| ||||| | ||
1437 ATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGGTCAAGC 1486

2401 CGGCGCGCCTGGGCTTCGCTGTAGCCCTGGTGTATGAACTCGCTCTGC 2450
    | | | ||||| |||| | | ||||| ||||| ||||| ||||| ||||
1487 CAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGTATGATGAATCCTTCTGT 1536

2451 TTCTGTGTGGTGGCGCGCGCTACATCAAGCTCTACTGTGACCTGCCACG 2500
    ||||| ||||| ||||| ||||| ||||| || ||||| ||||| || ||
1537 TTCTGTGTGGTGGCGCGGTGCCCTACATCAAACTGTACTGTGACCTGCCCGG 1586

2501 GGGTGACTTTGAGGCCGTGTGGGACTGGCCCATGGTGGCGCACGTGGCCT 2550
    ||| ||||| ||||| ||||| ||||| ||||| ||||| || ||||| ||
1587 GGGCGACTTTGAGGCCGTGTGGGACTGGCCCATGGTGTGAGGCACGTGGCCT 1636
```

2551 GGCTCATCTTTGCAGATGSCCTCCTCTACTGCCCGTGGCCCTTCCTCAGC 2600
||||| |||| | ||||| |||| | ||||| ||||| ||||| |||||
1637 GGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCC GTGGCCCTTCCTCAGC 1686

2601 TTTGCCCTCCATGCTGGGCCCTCTTCCCTGTCAACCCCGAGGCTGTCAAATC 2650
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1687 TTCGCCCTCCATGCTGGGCCCTCTTCCCTGTCAACCCCGAGGCGGTCAAATC 1736

2651 AGTCCCTCTGGTGCTGCCCTCTGCCCTGCCCTCAACCCACTGCTCT 2700
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1737 TGTCCTGCTGGTGCTGCCCTCTGCCCTGCCCTCAACCCACTGCTGT 1786

2701 ACCTGCTCTTCAACCCTCACTTCGGGATGACCTTCGGCGGCTCTGGCCA 2750
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1787 ACCTGCTCTTCAACCCCACTTCGGGATGACCTTCGGCGGCTTCGGCCC 1836

2751 AGCCCTCGTCCCCAGGGCCCCCTAGCCTACGCTGCAGCCGGTGAGCTGGA 2800
|| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1837 CGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGAGCTGGA 1886

2801 GAAGAGCTCCTGCGACTCCACCCAAAGCGCTGGTGGCTTCTCAGATGTGG 2850
||||| |||| | ||||| || ||||| || ||||| || ||||| || |||||
1887 GAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGG 1936

2851 ATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCCTGGGCTAGAGACC 2900
||| ||||| ||||| ||||| ||||| || ||||| || ||||| || |||||
1937 ATCTCATTTCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGGCTGGAGACC 1986

22901	TATGGCTTCCCTTCAGTGACCTCTCATCTCCCGACATCAGCCGGGGCCAC	2950
11987	TATGGCTTCCCTTCAGTGACCTCTCATCTCCTGTCTCAGCAGCCAGGGGCCCC	2036
22951	CAGGCTGGAGGGAACCATTTTATAGAGTCTGATGGAACCAAGTTGGGA	3000
22037	CAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGAACCACTTTGGGA	2086
23001	ACCCACAACCTCCCATGAAGGGAGAACTGCTGCTGAAGCAGAGGGAGCC	3050
22087	ACCCCCAACCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCT	2136
23051	ACTTTGGCAGGCTGTGGCTCTTCCGTGGTGAGCCCTCTGGCCCTCTGG	3100
22137	ACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGCGGCTTTTCAGCCCTCTGG	2186
23101	CTCTCTCTTTGCCCTCTCACTTGTAATAATCCCT	3133
22187	CTTGGCCTTTGCTTCACACGCTGTAATAATCCCTCCCCCATCTTCTCTCC	2236
23134	CTCTGTT...TGTC..CTCTCCCCATC...CAATGATGGCTGCTTATAA	3174
22237	CCCTCTCTCCCTTTCCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAA	2286
23175	AAGAAAGACAACTCCAAC.....TCCATAGCAAGATGGCCAAC	3212
22287	AACAAATACAAACCAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAG	2336

FIG. 12J

```
3550 GCTGNGCCAAAGTGCTTCCTGTAAATAACACTTTGGAAGACATTGAAA 3599
    || :|| || ||||| ||||| ||||| ||||| |||||
2652 GCCATGCATAAAGACTTCCTATTAAATAAGCTTTGGAAGAGATTAAAA 2701

3600 AAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3637
    ||||| |||||
2702 AAAAAAAAAA..... 2711
```

FIG. 13A

GAP of: FrGcgManager_102_MTA0uXMaE check: 8470 from: 1 to: 968
 mLGR6.aa (analysis only) - Import - complete
 to: FrGcgManager_102_NTAf7nCL_ check: 5092 from: 1 to: 737
 corrected hLGR6.aa (analysis onl - Import - complete
 Symbol comparison table: /prod/ddm/seganal/BLAST/matrix/aa/BLOSUM62
 CompCheck: 1102
 Matrix made by matblas from blosum62.iij

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248
Quality:	3424	Length:	968
Ratio:	4.646	Gaps:	0
Percent Similarity:	90.773	Percent Identity:	89.281

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	2
.	=	1

FIG. 13B

FrGcgManager_102_MTA0uXMaE x FrGcgManager_102_NTAf7nCl_ May 5, 19100 15:04

```

201 IPDYAFQNLTSVLVHLHNNRIQHVGTHSFEGHNLLETLDLNYNELQEEF 250
      .
      .
      .
1  .....GLHNLETLDLNYNKLQEEF 19
      .
      .
      .
251 LAIRTLGRLQELGFHNNNIKAPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
      .
      .
      .
20 VAIRTLGRLQELGFHNNNIKAPEKAFMGNPLLQTIHFYDNPIQFVGRSA 69
      .
      .
      .
301 FQYLSKLHTLSLNGATDIQEFFDLKGTTSLLEILTLTRAGIRLLPPGVCQQ 350
      .
      .
      .
70 FQYLPKLHTLSLNGAMDIQEFFDLKGTTSLLEILTLTRAGIRLLPSGMCQQ 119
      .
      .
      .
351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
      .
      .
      .
120 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 169
      .
      .
      .
401 QALDLSWNAIRAIHPEAFSTLRSVLKLDLTDNQLTTLPLAGLGGLMHLKL 450
      .
      .
      .
170 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 219
  
```

FIG. 13C

451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFCKTSQWQAEDF 500
|||||
220 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFCKASGQWEAEDL 269
501 HPEEEEEAPKRPLGLLAGQAEHNYDLDLDELQMGTEDSKPNPSVQCSPVPG 550
| : |||
270 HLDDEESSKRPLGLLARQAEHNYDQDLDLDELQLEMEDSKPHPSVQCSPTPG 319
551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLV 600
|||||
320 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 369
601 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 650
|||
370 VGAAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRTGFLAV 419
651 LGSEASVLLTLAAVQCSISVTCVRAYGKAPSPGSRAGALGCLALAGLA 700
|||||
420 LGSEASVLLTLAAVQCSVSVSCVRAYGKSPSLGSRAGVLGCLALAGLA 469
701 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMNSLCFLVVAGA 750
|||||
470 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMNSFCFLVVAGA 519
751 YIKLYCDLPRGDFEAVWDCAMVRHVAVWLIFADGLLYCPVAFLSFASMLGL 800
|||||
520 YIKLYCDLPRGDFEAVWDCAMVRHVAVWLIFADGLLYCPVAFLSFASMLGL 569

[illegible]

FIG. 14A

>15088
> Fbh150881 - Import - vector trimmed
CCGCCSGCGGTGCAGCCCGCGGACCGGAGCGGAGCTGCGGCCACCGCGCGTGCGG
TCGCGCGCCCGCGCCAGGTGCCCCAGTAGCCCGACCGCCGAGATGCCAGCCCGCGGG
GCTCCGGCGCTATGGCTTTGCGCGCGCTGTGCGCTTCCCGAGGGCCGCGCGCGCCCC
CCAGCCCGCGCGCGCCACCGCTGCCCGCGCGCCCTGCCACTGCCAGGAGGACGGCAT
CATGCTGTGCGGACTGCTGTAGCTCGGCTGTCCGCCGTTCCGGGGACCTGGACCC
CCTGACGGCTTACCTGGACCTCAGCATGAACAACCTCACAGAGCTTACGCTGGCCTCTT
CCACCACCTGCGCTTCTTGAGGAGCTGCGTCTCTCTGGGAACCATCTCTCACACATCCC
AGGACAAGCATTTCTTGGTCTCTACAGCCTGAAAATCTGATGCTGCAGAACAAATCAGCT
GGAGGAATCCCCGCAGAGCGCTGTGGGAGCTGCCGAGCTGCAGTGCCTGCCCTAGA
TGCCAAACCTCATCTCCCTGGTCCCGGAGAGAGCTTTGAGGGCTGTCTCCCTCCGCCA
CCTCTGGCTGGACGACAATGCACCTACCGAGATCCCTGTCAAGGGCCCTCAACAACCTCCC
TGCCCTGCAGGCCATGACCTGGCCCTCAACCGCATCAGCCACATCCCGACTACGCGTT
CCAGAACTCTCACCAGCCTTGTGTGTGCTGCATTTGCATAACAACCGCATCCAGCATCTGGG
GACCCACAGCTTCGAGGGCTGCACAATCTGGAGACACTAGACCTGAATTATAACAAGCT
GCAGGAGTTCCCTGTGGCCATCCGGACCTGGGCAGACTGCAGGAACCTCTGCTACAGACGAT
CAACAACATCAAGGCCATCCAGAAAAGGCCCTTCATGGGGAACCTCTGCTACAGACGAT
ACACTTTTATGATAACCCAAATCCAGTTTGTGGGAAGATCGGCATTCAGTACCTGCCCTAA
ACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGG
CACACACAGCTGAGATCCCTGACCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGGG
GATGTGCCAACAGCTGCCCGAGCTCCGAGTCCCTGGAACTGTCTCAAAATCGAGGA
GCTGCCAGCCTGCACAGGTGTCAAGAAATGGAGGAAATCGGCCCTCAACAACACCGCAT
CTGGGAAATTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAG
CTGGAACGCCATCCGGTCCATCCACCTGAGGCCCTTCTCCACCTGCACTCCCTGGTCAA
GCTGGACCTGACAGACAACAGCTGACCACACTGCCCTGGCTGSACTTGGGGGCTTGAT
GCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCTCCCGAGGCCCTTCTCCAAGGACAGTTTCCC

AAAACTGAGGATCCTGGAGGTGCCCTTATGCCCTACCAAGTGTCTCCCTATGGGATGTGTGC
CAGCTTCTTCAAGCCCTCTGGGCAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGA
GTCTTCAAAAAGGCCCTGGCCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGA
CCTGGATGAGCTCCAGCTGGAGATGGAGACTCAAAGCCACACCCAGTGTCCAGTGTAG
CCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAAGCTGGGGCATCCGCCCT
GGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTGCAATGGAATGGTGTGCTGCTGACCCGT
GTTGCGCTGGCGGCCCTGCCCCCTGCCCCCGGTCAAAGTTTGTGGTAGGTGCGATTGCAGG
CGCCAAACACCTTGACTGGCAATTCTCTGTGGCCCTTCTAGCCCTCAGTCGATGCCCTGACCTT
TGGTCAGTTCTCTGAGTACGGAGCCCGCTGGAGACGGGGCTAGGCTGCCGGGCCACTGG
CTTCCCTGGCAGTACTTTGGGTCTGGAGGCATCGGTGCTGTCTACTCTGGCCCGCAGTGCA
GTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGGGAAGTCCCCCTCCCTGGGCAGCGT
TCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCCCTGGC
CTCAGTGGGAGAAATACGGGGCTTCCCCACTCTGCCCTACGCGCCACCTGAGGGTCA
GCCAGCAGCCCTGGGCTTCAACGTGGCCCTGGTGATGATGAATCTCTTCTGTTTCTCTGGT
CGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCTGCCCGGGCGCACTTGTAGGCCGT
GTGGGACTGGCCCATGGTGAGGCACGTGGCCCTGGCTCATCTTCGCAGACGGGCTCCTCTA
CTGTCCCGTGGCCTTCCCTCAGCTTCGCCCTCCATGCTGGCCTCTTCCCTGTACGCCCGA
GGCCGTCAAGTCTGTCCCTGCTGGTGGTGTGCCCTGCCCTGCCCTCAACCCACTGCT
GTACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGG
GGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGGGAGCTGGAGAAAGAGCTCCTGTGATTCT
TACCCAGGCCCTGTAGCCTTCTCTGATGTGATCTCATTTCTGGAAGCTTCTGAAGCTGG
GGGCCCCCTGGGCTGGAGACCTATGGCTTCCCTCAGTGACCCCTCATCTCCTGTGTCAGCA
GCCAGGGGCCCCAGGCTGGAGGCGAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGG
GAACCCCAACCCCTCATGGATGGAGAACTGCTGTGAGGGCAGAGGGATCTACGCCAGC
AGGTGAGGCTTGTACGGGGTGGCGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTTCACA
CGTGTAAATATCCCTCCCATTTCTCTCTTCCCTCTCTTCCCTTCTCTCTCTCTCTCTCTCT
GGTGAATGATGGCTCTTCTAAAACAAATACAACCAAACTCAGCAGTGTGATCTATAGC

FIG. 14C

AGGATGGCCCAAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGT
GCCCTTGGCCCTGGCTTCCCTTGGCCCTTCCCTCAGCTTCACCTTGATACTGGGCCCTCTTC
CTTGTCATGCTGAAGCTGTGGACCARAGACCTGGACTTTTGTCTGCTTAAGGGAATGA
GGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATCAGGGCCACAGTGGACAGGGAGACCT
CACARAAAAAGGCCCTGGAAGGKGATTTCCCGTGTGACTCATGGRTAGGAWACAAAAATGTG
TTCATGTACCATTAATCTTGACATATGCCATGCATAAARACTTCCTATTAAAAATAAGCT
TTGGRAGAGATT

FIG. 15

>15088

MPSPPGLRALWLCALCASRRAGGAPQPGPGTACAPACHCQEDGIMLSADCSELGLSAVPGDLDPLTAYLDLSMNNLT
ELQPGLFHHLRLEELRLSGNHLSHIPGQAFSGLYSLKIIMLQNNQLGGIPAEALWELPSLSRLDANLISLVPERSE
EGLSSLRHLWLDNALTEIPVRALNNLPALQAMTLALNRI SHIPDYAFQNLTSLVVHLHNNRIQHLGTHSFEGLHNLE
TLDLNYNKLQEEFPVAIRTLGRQLQELGFHNNNIKAIPKAFMGNPLLTQTIHFYDNPIQFVGRSAFQYLPKLTLSLNGAM
DIQEFFDLKGTTSLEILTTLTRAGIRLLPSGMCQQPLRLRVLELSHNQIEELPSLHRCQKLEELGLQHNRIWEIGADTFS
QLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGIMHLKLGKGNLALSQAFSKDSFPKLRILEVP
YAYQCCPYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFK
PCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPVKFVVGAIAAGANTLTGISCGLLASVDALTFGQFSEY
GARWETGLCRATGFLAVLGSEASVLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCIALAGLAAALPLASVGEY
GASPLCLPYAPPEGQPAALGFTVALVMNNSFCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAVWLIFADGLLYCPVA
FLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLENPHFRDDLRRLLRPRAGDSGPLAYAAAGELEKSSCDSTQA
LVAFSDVDLILEASEAGRPPGLETYGFPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRLRAEGSTPAGG
GLSGGGGFGQPSGLAFASHV*

FIG. 16A

protein alignment between mouse and human
 > IGR6.

15088m(analysis only) - Import - complete

to: FrGcgManager_9_QBAsD4iW_ check: 8637 from: 1 to: 968

15088h(analysis only) - Import - complete

Symbol comparison table: /prod/ddm/seganal/BLAST/matrix/aa/BLOSUM62
 CompCheck: 1102

Matrix made by matblas from blosum62.iij

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248
Quality:	4495	Length:	968
Ratio:	4.653	Gaps:	2
Percent Similarity:	91.097	Percent Identity:	89.855

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	2
.	=	1

FrGcgManager_9_PBA0KkgfJ x FrGcgManager_9_QBAsD4iW_ March 15, 19101 15:24

FIG. 16B

1	MHSP	PGLL	ALWL	CAVL	CAS	ARGG	SDP	QPG	GR	PAC	PAC	HC	QED	GIM	LSA	50	Mouse																							
1	MPSP	PGLR	ALWL	CAAL	CAS	RRAG	GA	PQPG	PTAC	PAC	HC	QED	GIM	LSA	50	Human																								
51	DCSE	LGLS	VPAD	LDPL	TAYL	DL	SMNN	LTEL	QPG	LH	FR	FEEL	RL	SGN	100																									
51	DCSE	LGLS	AVPG	DLDP	L	TAYL	DL	SMNN	LTEL	QPG	LH	FR	FEEL	RL	SGN	100																								
101	HLSH	IPGQ	AFSG	LHSL	KILM	LQSN	QLRG	IPAE	ALWE	LP	SL	RL	DA	NLI	150																									
101	HLSH	IPGQ	AFSG	LYSL	KILM	LQNN	QLGG	IPAE	ALWE	LP	SL	RL	DA	NLI	150																									
151	SLVP	ERSF	EGLS	SLRH	LWDD	NALTEI	PV	RA	NNLP	AL	QA	MT	LA	LN	HIRH	200																								
151	SLVP	ERSF	EGLS	SLRH	LWDD	NALTEI	PV	RA	NNLP	AL	QA	MT	LA	LN	RISH	200																								
201	IPDY	AFQN	LTS	LV	VL	HL	HNNR	IQHV	GTHS	FE	GL	HN	LE	TLD	LN	YNEL	QEEF	250																						
201	IPDY	AFQN	LTS	LV	VL	HL	HNNR	IQHL	GTHN	FE	GL	HN	LE	P	LD	LN	YNKL	QEEF	250																					
251	LAIR	TGRL	QELG	FHNN	NIKA	IPEK	AF	MGN	PLLQ	TI	H	FYD	NP	IQ	FV	GRSA	300																							
251	VAIR	TGRL	QELG	FHNN	NIKA	IPEK	AF	MGN	PLLQ	TI	H	FYD	NP	IQ	FV	GRSA	300																							
301	FQYL	SKLH	TL	SL	NG	ATD	I	Q	E	F	P	D	L	K	G	T	S	L	E	I	L	T	L	T	R	A	G	I	R	L	L	P	P	G	V	C	Q	Q	350	
301	FQYL	PKLH	TL	SL	NG	AM	D	I	Q	E	F	P	D	L	K	G	T	S	L	E	I	L	T	L	T	R	A	G	I	R	L	L	P	S	G	M	C	Q	Q	350

FIG. 16C

351 LPRLRILELSHNQIEELPSLHRCQKLEELGLRHNRIKEIGADTFSQLGSL 400
||||:|||||||||||||||||||||||||||||||||||||
351 LPRLRVLELSHNQIEELPSLHRCQKLEELGLQHNRIWEIGADTFSQLSSL 400
401 QALDLSWNAIRAIHPEAFSTLRSVLKLDLTDNQLTTLPLAGLGGLMHLKL 450
|||||||||:|||||||||:|||||||||:|||||||||:||||
401 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASF FKTSGQWQAEDF 500
|||||||||:|||||||||:|||||||||:|||||||||:||||
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASF FKASGQWEAEDL 500
501 HPEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPG 550
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
501 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 550
551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNG.VLLTVFASGPSPLSP.KLV 598
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
551 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 600
599 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 648
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
601 VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV 650
649 LGSEASVLLLTAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA 698
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
651 LGSEASVLLLTAAVQCSVSVSCVRAYGKSPSLGSLGVRAGVLGCLALAGLA 700

